



SEQUENCE LISTING

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<120> RNA Polymerase

<130> 024705-077

<140> US 09/254,344

<141> 1999-09-03

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<151> 1998-07-06

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<151> 1998-06-04

<160> 39

<170> PatentIn version 3.0

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Glu Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu
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99

cgt tta gct cgc gaa cag ttg gcc ctt gag cat gag tct tac gag atg
Arg Leu Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met
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147

ggt gaa gca cgc ttc cgc aag atg ttt gag cgt caa ctt aaa gct ggt
Gly Glu Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly
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195

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Glu Val Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu
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243

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291

RECEIVED

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act atg gtt gac aca tat gag tct tgt gat gta ctg gct gat ttc tac	2547
Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr	
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Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro	
850 855 860	
gca ctt ccg gct aaa ggt aac ttg aac ctc cgt gac atc tta gag tcg	2643
Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser	
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35 40 45	
Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val	
50 55 60	
Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys	
65 70 75 80	
Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg	
85 90 95	
Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu	
100 105 110	
Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser	
115 120 125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
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Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
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Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
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Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
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Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
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Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
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Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
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Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
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Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
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His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
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Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
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Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
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Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
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Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
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Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
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Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700

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Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
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Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765

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 770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
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Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
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Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Lys Met Ile Ala
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Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg Gly Lys Arg
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Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu Ala Val Ala
 100 105 110

Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser Ala Asp Asn
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Thr Thr Val Gln Ala Ala Ile Gly Arg Ala Ile Glu Asp Glu Ala Arg
 130 135 140

Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys His Phe Lys Lys Asn Val
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Glu Glu Gln Leu Asn Lys Arg Val Gly His Val Tyr Lys Ala Phe
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Met Gln Val Val Glu Ala Asp Met Leu Ser Lys Gly Leu Leu Gly Gly
 180 185 190

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 195 200 205

Arg Met Leu Ile Glu Ser Thr Gly Met Val Ser Leu His Arg Gln Asn
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Lys Val Leu Ala Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro
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Glu Asp Ile Asp Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala
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Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys
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Val Ser Met Phe Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala
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Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His
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Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile
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Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser
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Pro Leu Glu Asn Thr Ile Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala
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Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr Asn
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Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln His
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Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys Lys
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Val Asn Glu Ile Leu Gln Ala Asn Gly Thr Asp Asn Glu Val Val Thr
 565 570 575

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Ser Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys
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 35 40 45
 Glu Arg Arg Phe Leu Lys Met Leu Glu Arg Gln Ala Lys Ala Gly Glu
 50 55 60
 Ile Ala Asp Asn Ala Ala Lys Pro Leu Leu Ala Thr Lys Leu Thr
 65 70 75 80
 Thr Arg Ile Val Glu Trp Leu Glu Glu Tyr Ala Ser Lys Lys Gly Arg
 85 90 95
 Lys Pro Ser Ala Tyr Ala Pro Leu Gln Leu Leu Lys Pro Glu Ala Ser
 100 105 110
 Ala Phe Ile Thr Leu Lys Val Ile Leu Ala Ser Leu Thr Ser Thr Asn
 115 120 125
 Met Thr Thr Ile Gln Ala Met Leu Gly Lys Ala Ile Glu Asp Glu Ala
 130 135 140
 Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys His Phe Lys Lys His
 145 150 155 160
 Val Glu Glu Gln Leu Asn Lys Arg His Gly Gln Val Tyr Lys Lys Ala
 165 170 175
 Phe Met Gln Val Val Glu Ala Asp Met Ile Gly Arg Gly Leu Leu Gly
 180 185 190
 Gly Glu Ala Trp Ser Ser Trp Asp Lys Glu Thr Thr Met His Val Gly
 195 200 205
 Ile Arg Met Leu Ile Glu Ser Thr Gly Leu Val Glu Leu Gln Arg His
 210 215 220
 Asn Ala Gly Asn Ala Gly Ser Asp His Glu Ala Leu Gln Leu Ala Gln
 225 230 235 240
 Glu Tyr Val Asp Val Leu Ala Lys Ala Gly Ala Leu Ala Gly Ile Ser
 245 250 255
 Pro Met Phe Gln Pro Cys Val Val Pro Pro Lys Pro Trp Val Ala Ile
 260 265 270
 Thr Gly Gly Tyr Trp Ala Asn Gly Leu Ala Leu Val Arg Thr His

275	280	285
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290	295	300
Tyr Lys Ala Val Asn Leu Ala Gln Asn Thr Ala	Trp Lys Ile Asn Lys	
305	310	315
Lys Val Leu Ala Val Val Asn Glu Ile Val Asn Trp	Lys Asn Cys Pro	
325	330	335
Val Ala Asp Ile Pro Ser Leu Glu Arg Gln Glu Leu	Pro Pro Lys Pro	
340	345	350
Asp Asp Ile Asp Thr Asn Glu Ala Ala Leu Lys	Glu Trp Lys Lys Ala	
355	360	365
Ala Ala Gly Ile Tyr Arg Leu Asp Lys Ala Arg	Val Ser Arg Arg Ile	
370	375	380
Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys	Phe Ala Ser Lys Lys	
385	390	395
Ala Ile Trp Phe Pro Tyr Asn Met Asp	Trp Arg Gly Arg Val	Tyr Ala
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Val Pro Met Phe Gly Asn Asp Met Thr Lys Gly	Leu Leu Thr Leu Ala	
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Lys Gly Lys Pro Ile Gly Glu Glu Gly Phe	Tyr Trp Leu Lys Ile His	
435	440	445
Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro	Phe Pro Glu Arg Ile	
450	455	460
Ala Phe Ile Glu Lys His Val Asp Asp Ile	Leu Ala Cys Ala Lys Asp	
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Pro Ile Asn Asn Thr Trp Trp Ala Glu Gln Asp	Ser Pro Phe Ala Phe	
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Cys Phe Glu Tyr Ala Gly Val Thr His His Gly	Leu Ser Tyr Asn Cys	
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Ser Ala Met Leu Arg Asp Glu Val Gly Gly	Arg Ala Val Asn Leu	Leu
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Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly	Ile Val Ala Gln Lys	Val
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Thr Asp Lys Asp Thr Gly Glu Ile Ser Glu Lys	Leu Lys Leu Gly Thr	
580	585	590

Fig 8b

Ser Thr Leu (Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val
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Thr Lys Arg Ser Val (Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly
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Ile Trp Asp Ala Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met
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 740 745 750

Pro Asn Phe Val His Ser Gln Asp Gly Ser Arg Leu Met Thr Val Val
 755 760 765

Tyr Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp
 770 775 780

Ser Phe Gly Thr Ile Pro Gly Lys Leu Phe Lys Ala Val Arg Glu Thr
 785 790 795 800

Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser
 805 810 815

Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro
 820 825 830

Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp
 835 840 845

Phe Ala Phe Ala
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<210> 5
 <211> 876
 <212> PRT
 <213> Bacteriophage K11

<400> 5
 Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu

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			20				25			30					
Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ala	Tyr	Glu	Leu	Gly	Arg
			35			40			45						
Gln	Arg	Phe	Leu	Lys	Met	Leu	Glu	Arg	Gln	Val	Lys	Ala	Gly	Glu	Phe
			50			55			60						
Ala	Asp	Asn	Ala	Ala	Ala	Lys	Pro	Leu	Val	Leu	Thr	Gln	Leu	Thr	Lys
			65			70			75			80			
Arg	Ile	Asp	Asp	Trp	Lys	Glu	Gln	Ala	Asn	Ala	Arg	Gly	Lys	Lys	
			85			90			95						
Pro	Arg	Ala	Tyr	Tyr	Pro	Ile	Lys	His	Gly	Val	Ala	Ser	Glu	Leu	Ala
			100			105			110						
Val	Ser	Met	Gly	Ala	Glu	Val	Leu	Lys	Glu	Lys	Arg	Gly	Val	Ser	Ser
			115			120			125						
Glu	Ala	Ile	Ala	Leu	Leu	Thr	Ile	Lys	Val	Val	Leu	Gly	Asn	Ala	His
			130			135			140						
Arg	Pro	Leu	Lys	Gly	His	Asn	Pro	Ala	Gln	Leu	Gly	Lys	Ala	Leu	Glu
			145			150			155			160			
Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Glu	Gln	Glu	Ala	Ala	Tyr	Phe
			165			170			175						
Lys	Lys	Asn	Val	Ala	Asp	Gln	Leu	Asp	Lys	Arg	Val	Gly	His	Val	Tyr
			180			185			190						
Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Ile	Ser	Lys	Gly
			195			200			205						
Met	Leu	Gly	Gly	Asp	Asn	Trp	Ala	Ser	Trp	Lys	Thr	Asp	Glu	Gln	Met
			210			215			220						
His	Val	Gly	Thr	Lys	Leu	Leu	Ile	Glu	Gly	Thr	Gly	Leu	Val	Glu	Met
			225			230			235			240			
Thr	Lys	Asn	Lys	Met	Ala	Asp	Gly	Ser	Asp	Asp	Val	Thr	Ser	Met	Gln
			245			250			255						
Met	Val	Gln	Leu	Ala	Pro	Ala	Phe	Val	Glu	Leu	Leu	Ser	Lys	Arg	Ala
			260			265			270						
Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	His	Gln	Pro	Cys	Val	Val	Pro
			275			280			285						
Pro	Lys	Pro	Trp	Val	Glu	Thr	Val	Gly	Gly	Tyr	Trp	Ser	Val	Gly	
			290			295			300						
Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Arg	Arg	Tyr	Ala
			305			310			315			320			

Asp Val His Met Pro Glu Val Tyr Lys Ala Val Asn Leu Ala Gln Asn
 325 330 335
 Thr Pro Trp Lys Val Asn Lys Lys Val Leu Ala Val Val Asn Glu Ile
 340 345 350
 Val Asn Trp Lys His Cys Pro Val Gly Asp Val Pro Ala Ile Glu Arg
 355 360 365
 Glu Glu Leu Pro Pro Arg Pro Asp Asp Ile Asp Thr Asn Glu Val Ala
 370 375 380
 Arg Lys Ala Trp Arg Lys Glu Ala Ala Ala Val Tyr Arg Lys Asp Lys
 385 390 395 400
 Ala Arg Gln Ser Arg Arg Cys Arg Cys Glu Phe Met Val Ala Gln Ala
 405 410 415
 Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp
 420 425 430
 Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe Gly Asn Asp Met Thr
 435 440 445
 Lys Gly Ser Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Leu Asp Gly
 450 455 460
 Phe Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys
 465 470 475 480
 Val Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn Glu Gly Asn
 485 490 495
 Ile Leu Ala Ser Ala Ala Asp Pro Leu Asn Thr Trp Trp Thr Gln Gln
 500 505 510
 Asp Ser Pro Phe Ala Phe Cys Phe Glu Tyr Ala Gly Val Lys His His
 515 520 525
 Gly Leu Asn Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser
 530 535 540
 Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly
 545 550 555 560
 Gly Arg Ala Val Asn Leu Leu Pro Ser Asp Thr Val Asp Ile Tyr Lys
 565 570 575
 Ile Val Ala Asp Lys Val Asn Glu Val Leu His Gln Asn Gly Ser Gln
 580 585 590
 Thr Val Val Glu Gln Ile Ala Asp Lys Glu Thr Gly Glu Phe His Glu
 595 600 605
 Lys Val Thr Leu Gly Glu Ser Val Leu Ala Ala Gly Gln Trp Leu Gln
 610 615 620
 Tyr Gly Val Thr Arg Lys Val Thr Lys Arg Ser Val Met Thr Leu Ala
 625 630 635 640

Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln Gln Val Leu Glu Asp Thr
 645 650 655
 Ile Gln Pro Ala Ile Asp Asn Gly Glu Phe Thr His Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Asp Ala Ser Thr Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Gly Val Ile Leu His
 705 710 715 720
 Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp Gln
 725 730 735
 Glu Gln Asn Gln Ala Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn
 740 745 750
 Val Lys Met Thr Tyr Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His
 755 760 765
 Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 770 775 780
 Ser His Leu Arg Met Thr Val Val His Ala Asn Glu Val Tyr Gly Ile
 785 790 795 800
 Asp Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro Gly Asn
 805 810 815
 Leu Phe Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn
 820 825 830
 Asp Val Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu
 835 840 845
 Ser Gln Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn
 850 855 860
 Leu Arg Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala
 865 870 875
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 <211> 841
 <212> PRT
 <213> Bacteriophage SP6
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 20 25 30
 Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu

35	40	45	
Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys Glu Glu Tyr Glu Gly Lys			
50	55	60	
Lys Gly Arg Ala Pro Arg Ala Leu Ala Phe Leu Gln Cys Val Glu Asn			
65	70	75	80
Glu Val Ala Ala Tyr Ile Thr Met Lys Val Val Met Asp Met Leu Asn			
85	90	95	
Thr Asp Ala Thr Leu Gln Ser Val Ala Glu Arg Ile Glu Asp Gln Val			
100	105	110	
Arg Phe Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe Glu Lys Val			
115	120	125	
Lys Lys Ser Leu Lys Ala Ser Arg Thr Lys Ser Tyr Arg His Ala His			
130	135	140	
Asn Val Ala Val Val Ala Glu Lys Ser Val Ala Glu Lys Asp Ala Asp			
145	150	155	160
Phe Asp Arg Trp Glu Ala Trp Pro Lys Glu Thr Gln Leu Gln Ile Gly			
165	170	175	
Thr Thr Ile Leu Glu Gly Ser Val Phe Tyr Asn Gly Glu Pro Val Phe			
180	185	190	
Met Arg Ala Met Arg Thr Tyr Gly Gly Lys Thr Ile Tyr Tyr Leu Gln			
195	200	205	
Thr Ser Glu Ser Val Gly Gln Trp Ile Ser Ala Phe Lys Glu His Val			
210	215	220	
Ala Gln Leu Ser Pro Ala Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro			
225	230	235	240
Trp Arg Thr Pro Phe Asn Gly Gly Phe His Thr Glu Lys Val Ile Arg			
245	250	255	
Leu Val Lys Gly Asn Arg Glu His Val Arg Lys Leu Thr Gln Lys Gln			
260	265	270	
Met Pro Lys Val Tyr Lys Ala Ile Asn Ala Leu Gln Asn Thr Gln Trp			
275	280	285	
Gln Ile Asn Lys Asp Val Leu Ala Val Ile Glu Glu Val Ile Arg Leu			
290	295	300	
Asp Leu Gly Tyr Gly Val Pro Ser Phe Lys Pro Leu Ile Asp Lys Glu			
305	310	315	320
Asn Lys Pro Ala Asn Pro Val Pro Val Glu Leu Arg Gly Arg Glu Leu			
325	330	335	
Lys Glu Met Leu Ser Pro Glu Gln Trp Gln Gln Phe Ile Asn Trp Lys			
340	345	350	

Gly Glu Cys Ala Arg Leu Tyr Thr Ala Glu Thr Lys Arg Gly Ser Lys
 355 360 365
 Ser Ala Ala Val Val Arg Met Val Gly Gln Ala Arg Lys Tyr Ser Ala
 370 375 380
 Phe Glu Ser Ile Tyr Phe Val Tyr Ala Met Asp Ser Arg Ser Arg Val
 385 390 395 400
 Tyr Val Gln Ser Ser Thr Leu Ser Asn Asp Leu Gly Lys Ala Leu Leu
 405 410 415
 Arg Phe Thr Glu Gly Arg Pro Val Asn Gly Val Glu Ala Leu Lys Trp
 420 425 430
 Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys Lys Thr Phe
 435 440 445
 Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln Asp Met Cys
 450 455 460
 Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp Ala Lys Ala
 465 470 475 480
 Asp Ala Pro Tyr Ala Trp Cys Phe Glu Tyr Ala Gln Tyr Leu Asp Leu
 485 490 495
 Val Asp Glu Gly Arg Ala Asp Glu Phe Arg Thr His Leu Pro Val His
 500 505 510
 Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu Arg
 515 520 525
 Asp Glu Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp Ala Pro
 530 535 540
 Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Asn Ala Leu Tyr
 545 550 555 560
 Met Asp Ala Asp Asp Ala Thr Thr Phe Thr Ser Gly Ser Val Thr Leu
 565 570 575
 Ser Gly Thr Glu Leu Arg Ala Met Ala Ser Ala Trp Asp Ser Ile Gly
 580 585 590
 Ile Thr Arg Ser Leu Thr Lys Lys Pro Val Met Thr Leu Pro Tyr Gly
 595 600 605
 Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr Ile Val Asp
 610 615 620
 Leu Glu Glu Lys Glu Ala Gln Lys Glu Gly Arg Thr Ala Asn Lys Val
 625 630 635 640
 His Pro Phe Glu Asp Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 645 650 655
 Tyr Asn Tyr Met Thr Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val
 660 665 670

Lys Ala Pro Ile Val Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe
 675 680 685
 Ala Ala Lys Arg Asn Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe
 690 695 700
 Ile Leu Glu Gln Lys Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met
 705 710 715 720
 Gly Asp Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu
 725 730 735
 Ala Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp
 740 745 750
 Ala Ser His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val
 755 760 765
 Thr Ser Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Leu Thr
 770 775 780
 Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp Gly
 785 790 795 800
 Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met Val
 805 810 815
 Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu
 820 825 830
 Ile Met Asp Ser Glu Tyr Val Phe Ala
 835 840

<210> 7
 <211> 78
 <212> PRT
 <213> Bacteriophage T7

<400> 7
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15
 Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30
 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45
 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60
 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 8
 <211> 78
 <212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F644Y.

<400> 8

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 9

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F646Y.

<400> 9

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 10

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10
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 1 5 10 15
 Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30
 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro
 35 40 45
 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60
 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 11
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<400> 11
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 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60
 Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 12
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)...(73)
 <223> Mutant T7 RNA polymerase F644Y.
 <400> 12
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 1 5 10 15
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln
 20 25 30
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly

35

40

45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 13
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
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 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13
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 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 14
 <211> 73
 <212> PRT
 <213> Bacteriophage T3

<400> 14
 Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
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Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Asp Ala Val Ser Val Thr Val
 65 70

<210> 15
 <211> 73

<212> PRT
 <213> Bacteriophage K11

<400> 15
 Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg
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 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly
 60
 Leu Met (Phe) Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 Ile Trp Asp Ala Val Thr Val Val
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<210> 16
 <211> 75
 <212> PRT <
 <213> Bacteriophage SP6

<400> 16
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 Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu
 20 25 30
 Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys
 35 40 45
 Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp
 50 55 60
 Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 65 70 75

<210> 17
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 <212> DNA
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<220>
 <221> misc_feature
 <222> (1)..(31)
 <223> Mutant T7 RNA polymerase wild type.

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17
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<210> 18
<211> 32
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(32)
<223> Mutant T7 RNA polymerase wild type.

<220>
<221> misc_feature
<222> (1)..(32)
<223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18
gcgtcnnnaa aacgcacntt ttctntcgtn gg 32

<210> 19
<211> 19
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(19)
<223> Mutant T7 RNA polymerase F644Y.

<400> 19
cgaggggggg ccggtagccc 19

<210> 20
<211> 25
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(25)
<223> Mutant T7 RNA polymerase F644Y.

<220>
<221> misc_feature
<222> (6)..(6)
<223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20
ccccnttttg ttccttttagt gaggt 25

<210> 21
<211> 18
<212> DNA
<213> Bacteriophage T7

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<220>
 <221> misc_feature
 <222> (1)..(18)
 <223> Mutant T7 RNA polymerase F667Y.

 <400> 21
 gagggggggcc ggtaacgc 18

<210> 22
 <211> 22
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(22)
 <223> Mutant T7 RNA polymerase F667Y.

 <400> 22
 acgccttttg ttcccttttag tg 22

<210> 23
 <211> 569
 <212> DNA
 <213> Bacteriophage T7
 <220>
 <221> misc_feature
 <222> (1)..(569)
 <223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

 <220>
 <221> misc_feature
 <222> (1)..(472)
 <223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7
 5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"
 wherein "n" = any nucleotide

<400> 23
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 attatatac tnattagaca gnaaaatctn acccagntaa gacttctgga ggtttggtag 180
 agtagtttgt ctggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca 240
 cacttcagct taaaccaaca ggataggaaa aataggagc aacatggagt ggcattcctgg 300
 tatttctaca gtcctgtaga tgaagtctct atatgtgcaa catcctggga cagagcatat 360
 ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatggtag 420
 tggtgatgg tagcaataan cacactctct ccttcgatg tgcattgtat antcaggtgg 480
 atacaaaaag acatcgcttg gcccacatgc aaggccaaaa agcagacatc agaaagagag 540
 cagtcatgtg gggaaattgg tccgactgc 569

<210> 24		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> T7Rpol-N primer		
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<210> 25		
<211> 40		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> T7Rpol-C primer		
<400> 25		
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<210> 26		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> F646Y(+) primer		
<400> 26		
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<210> 27		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> F646Y(-) primer		
<400> 27		
gtccaaagag tacggcttcc gtcaac	26	
<210> 28		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> T7RNAP-HpaI-N primer		
<400> 28		
cgcgcggta acttgcttcc tag	23	
<210> 29		
<211> 23		
<212> DNA		
<213> Artificial Sequence		

<220>
<223> pTrc99a-PstI-C primer

<400> 29
gcatgcctgc aggtcgactc tag 23

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> ApaF1 primer

<400> 30
catctggtcg cattgggtca c 21

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Xho-R primer

<400> 31
ccaaagtgttc tcgagtgagg a 21

<210> 32
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Xho-F primer

<400> 32
ctaaagtctcc actcgagaac acttgg 26

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> AfIII-R primer

<400> 33
cagccagcag cttagcagca g 21

<210> 34
<211> 21
<212> DNA
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<220>
<223> 667R primer

<400> 34

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<210> 36	
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<212> DNA	
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<223> T7-DOUBLE-R primer	
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<210> 37	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
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<223> T7-DOUBLE-F primer	
<400> 37	
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<210> 38	
<211> 19	
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<213> Artificial Sequence	
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<223> L220 primer	
<400> 38	
caatttcaca cagaaaca	19
<210> 39	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
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<223> 1211 primer	
<400> 39	
acgttgtaaa acgacggcca gt	22